

RAW SEQUENCE LISTING

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Application Serial Number: 10/799, 417 A
Source: IFW16
Date Processed by STIC: 10/12/2005

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IFW16

RAW SEQUENCE LISTING

DATE: 10/12/2005

PATENT APPLICATION: US/10/799,417A

TIME: 11:25:33

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Output Set: N:\CRF4\10122005\J799417A.raw

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3 <110> APPLICANT: KRIEG, PAUL A.
5 <120> TITLE OF INVENTION: METHODS FOR MODULATING ANGIOGENESIS WITH APELIN
6   COMPOSITIONS
8 <130> FILE REFERENCE: 20825-0004
10 <140> CURRENT APPLICATION NUMBER: 10/799,417A
11 <141> CURRENT FILING DATE: 2004-03-12
13 <150> PRIOR APPLICATION NUMBER: 60/454,034
14 <151> PRIOR FILING DATE: 2003-03-12
16 <150> PRIOR APPLICATION NUMBER: 60/528,155
17 <151> PRIOR FILING DATE: 2003-12-09
19 <160> NUMBER OF SEQ ID NOS: 21
21 <170> SOFTWARE: PatentIn Ver. 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 77
25 <212> TYPE: PRT
26 <213> ORGANISM: Homo sapiens
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30   1           5           10           15
32 Leu Thr Ala Val Cys Gly Gly Ser Leu Met Pro Leu Pro Asp Gly Asn
33           20           25           30
35 Gly Leu Glu Asp Gly Asn Val Arg His Leu Val Gln Pro Arg Gly Ser
36           35           40           45
38 Arg Asn Gly Pro Gly Pro Trp Gln Gly Gly Arg Arg Lys Phe Arg Arg
39           50           55           60
41 Gln Arg Pro Arg Leu Ser His Lys Gly Pro Met Pro Phe
42   65           70           75
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46 <211> LENGTH: 36
47 <212> TYPE: PRT
48 <213> ORGANISM: Homo sapiens
50 <400> SEQUENCE: 2
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55           20           25           30
57 Pro Met Pro Phe
58           35
61 <210> SEQ ID NO: 3
62 <211> LENGTH: 17
63 <212> TYPE: PRT
64 <213> ORGANISM: Homo sapiens
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67 Lys Phe Arg Arg Gln Arg Pro Arg Leu Ser His Lys Gly Pro Met Pro
68 1 5 10 15
70 Phe
73 <210> SEQ ID NO: 4
74 <211> LENGTH: 13
75 <212> TYPE: PRT
76 <213> ORGANISM: Homo sapiens
78 <400> SEQUENCE: 4
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80 1 5 10
83 <210> SEQ ID NO: 5
84 <211> LENGTH: 13
85 <212> TYPE: PRT
86 <213> ORGANISM: Brachydanio rerio
88 <400> SEQUENCE: 5
89 Pro Arg Pro Arg Leu Ser His Lys Gly Pro Met Pro Phe
90 1 5 10
93 <210> SEQ ID NO: 6
94 <211> LENGTH: 25
95 <212> TYPE: DNA
96 <213> ORGANISM: Artificial Sequence
98 <220> FEATURE:
99 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
100 primer
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103 gtgcccaaag tctgagattc atgtt 25
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107 <211> LENGTH: 25
108 <212> TYPE: DNA
109 <213> ORGANISM: Artificial Sequence
111 <220> FEATURE:
112 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
113 primer
115 <400> SEQUENCE: 7
116 gattcatgtt tcttgtggct gagtg 25
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121 <212> TYPE: DNA
122 <213> ORGANISM: Artificial Sequence
124 <220> FEATURE:
125 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
126 oligonucleotide
128 <400> SEQUENCE: 8
129 gattgatctt tgttgtgcct cagtg 25
132 <210> SEQ ID NO: 9
133 <211> LENGTH: 25
134 <212> TYPE: DNA
135 <213> ORGANISM: Artificial Sequence
137 <220> FEATURE:

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138 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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150 <220> FEATURE:
151 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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155 aagcctctgt gcaaccaata caaag                25
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165     consensus sequence
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174 <213> ORGANISM: Homo sapiens
176 <400> SEQUENCE: 12
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183 <213> ORGANISM: Artificial Sequence
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186 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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190 cagacgtgac a                              11
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208 <212> TYPE: DNA

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219 <210> SEQ ID NO: 16
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222 <213> ORGANISM: Artificial Sequence
224 <220> FEATURE:
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233 <211> LENGTH: 380
234 <212> TYPE: PRT
235 <213> ORGANISM: Homo sapiens
237 <400> SEQUENCE: 17
238 Met Glu Glu Gly Gly Asp Phe Asp Asn Tyr Tyr Gly Ala Asp Asn Gln
239   1          5          10          15
241 Ser Glu Cys Glu Tyr Thr Asp Trp Lys Ser Ser Gly Ala Leu Ile Pro
242          20          25          30
244 Ala Ile Tyr Met Leu Val Phe Leu Leu Gly Thr Thr Gly Asn Gly Leu
245          35          40          45
247 Val Leu Trp Thr Val Phe Arg Ser Ser Arg Glu Lys Arg Arg Ser Ala
248          50          55          60
250 Asp Ile Phe Ile Ala Ser Leu Ala Val Ala Asp Leu Thr Phe Val Val
251          65          70          75          80
253 Thr Leu Pro Leu Trp Ala Thr Tyr Thr Tyr Arg Asp Tyr Asp Trp Pro
254          85          90          95
256 Phe Gly Thr Phe Phe Cys Lys Leu Ser Ser Tyr Leu Ile Phe Val Asn
257          100         105         110
259 Met Tyr Ala Ser Val Phe Cys Leu Thr Gly Leu Ser Phe Asp Arg Tyr
260          115         120         125
262 Leu Ala Ile Val Arg Pro Val Ala Asn Ala Arg Leu Arg Leu Arg Val
263          130         135         140
265 Ser Gly Ala Val Ala Thr Ala Val Leu Trp Val Leu Ala Ala Leu Leu
266          145         150         155         160
268 Ala Met Pro Val Met Val Leu Arg Thr Thr Gly Asp Leu Glu Asn Thr
269          165         170         175
271 Thr Lys Val Gln Cys Tyr Met Asp Tyr Ser Met Val Ala Thr Val Ser
272          180         185         190
274 Ser Glu Trp Ala Trp Glu Val Gly Leu Gly Val Ser Ser Thr Thr Val
275          195         200         205
277 Gly Phe Val Val Pro Phe Thr Ile Met Leu Thr Cys Tyr Phe Phe Ile
278          210         215         220
280 Ala Gln Thr Ile Ala Gly His Phe Arg Lys Glu Arg Ile Glu Gly Leu

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281 225          230          235          240
283 Arg Lys Arg Arg Arg Leu Leu Ser Ile Ile Val Val Leu Val Val Thr
284          245          250          255
286 Phe Ala Leu Cys Trp Met Pro Tyr His Leu Val Lys Thr Leu Tyr Met
287          260          265          270
289 Leu Gly Ser Leu Leu His Trp Pro Cys Asp Phe Asp Leu Phe Leu Met
290          275          280          285
292 Asn Ile Phe Pro Tyr Cys Thr Cys Ile Ser Tyr Val Asn Ser Cys Leu
293          290          295          300
295 Asn Pro Phe Leu Tyr Ala Phe Phe Asp Pro Arg Phe Arg Gln Ala Cys
296 305          310          315          320
298 Thr Ser Met Leu Cys Cys Gly Gln Ser Arg Cys Ala Gly Thr Ser His
299          325          330          335
301 Ser Ser Ser Gly Glu Lys Ser Ala Ser Tyr Ser Ser Gly His Ser Gln
302          340          345          350
304 Gly Pro Gly Pro Asn Met Gly Lys Gly Gly Glu Gln Met His Glu Lys
305          355          360          365
307 Ser Ile Pro Tyr Ser Gln Glu Thr Leu Val Val Asp
308          370          375          380
311 <210> SEQ ID NO: 18
312 <211> LENGTH: 14
313 <212> TYPE: PRT
314 <213> ORGANISM: Rana sp.
316 <400> SEQUENCE: 18
317 Arg Gln Arg Pro Arg Leu Ser His Lys Gly Pro Met Pro Phe
318 1          5          10
321 <210> SEQ ID NO: 19
322 <211> LENGTH: 14
323 <212> TYPE: PRT
324 <213> ORGANISM: Artificial Sequence
326 <220> FEATURE:
327 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
328 consensus sequence
330 <400> SEQUENCE: 19
331 Arg Gln Arg Pro Arg Leu Ser His Lys Gly Pro Met Pro Phe
332 1          5          10
335 <210> SEQ ID NO: 20
336 <211> LENGTH: 4
337 <212> TYPE: PRT
338 <213> ORGANISM: Artificial Sequence
340 <220> FEATURE:
341 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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344 <400> SEQUENCE: 20
345 Lys Lys Lys Arg
346 1
349 <210> SEQ ID NO: 21
350 <211> LENGTH: 4
351 <212> TYPE: PRT

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VERIFICATION SUMMARY

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